

FIGURE 1A

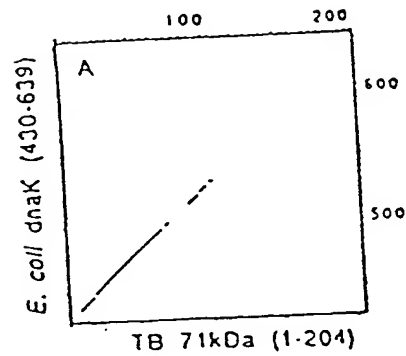
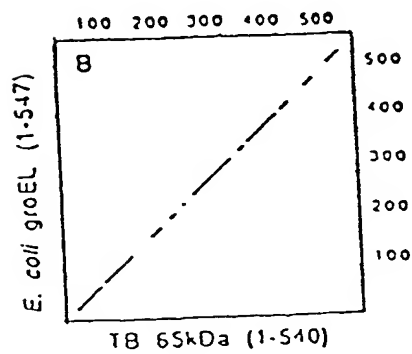


FIGURE 1B



	1	10	20	30	40	50	60	70
UMP1	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEEQSWGS							
GROEL	-----MA-----AKDVKFGNDARVKMLRGVNVVLADAVKVTLGPKGRNVVLDKSFGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATVLAARSIAKEGFEXISKGANPVEI							
GROEL	PTITKDGVSVAEIEPEDKFENMGAQMVKEVASKANDAAGDGTATVLAQAIITEGLKAVAAGMNPMDL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE							
GROEL	KRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETGVKLI AEAMDKVGKEGVITVEDGTGLQDE							
	211	220	230	240	250	260	270	280
HUMP1	LEIIEGMKFDRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANAHKPLVITAEVDVG							
GROEL	LDVVEGMQFDRGYLSPYFINKPETGAVELESFILLADKKISNIREMLPVLEAVAKAGKPLIIAEVDVG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVGLQVVAVKAPGFGDNRNKQLKDMAIATGGAVFGEEGLTNLEDVQPHDLGKVGEVIV							
GROEL	EALATAVVNTIRGIVKVA AVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLEDLGQAKRVVI							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNRLAKLSGDGVAVLKVGGTSDVEVNEKKDF							
GROEL	NKDTTTIIDGVGEEAAIQGRVAQIROQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKA							
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIRKTLKIPAMTIKNAGVEGSL							
GROEL	VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEQQNVVSSSL-RAMEAPLRQIVLNCGEPSV							
	491	500	510	520	530	540	550	56
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMS							
GROEL	ANTVKGGDGNVGYNAATEEYGNMIDMGILDPTKVTRSA LQYAASVAGLNIITECMVTDLPKND-AADLG							
	561	570						
HUMP1	MGGHGG--GMGGGMF							
GROEL	AGGHGGMGGMGGMM-							

Total score = 4667, 5 breaks
 276 identities out of 545 possible matches between residues

25 random runs
 Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGV	DLLADAVAVTMGPKGRTV	IEQSWGS					
HL65K	M-----	AKTIAYDEEARRGLERGLNSLADAVKVT	LGPKGRNVVLEKKWGA					
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGD	GGTTTATV	LARSIAKEGF	EKISKGANPVEI				
HL65K	PTITNDGV	SIAKEIELED	PEYKIGAELVKEVAKKTDDVAGD	GGTTTATV	LAQALVKEGLRNVAAGANPLGL			
	141	150	160	170	180	190	200	210
HUMP1	RRGVHLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKD	GKTLNDE						
HL65K	KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQSIGDLIAEAMD	KVGN	EGVITVEESNTFGLQ					
	211	220	230	240	250	260	270	280
HUMP1	LEIIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAH	RKPLV	IIAEDVDG					
HL65K	LELTEGMRFDKGYISGYFVTD	AERQZAVLEEPYILLVSSKVSTVKDLLP	LLKVIQAGKSLIIAEDVEG					
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNLRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLT	NLEDVQPHDLGKVGEVIV						
HL65K	EALSTLVN	KIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGAQVISEE-VGLT	LENTDLSLLGKARKVVM					
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGKGDKAQIEKRIQEIIIEQLDVTTSEYEKEKLN	ERLAKLS	DGVAVLKVGGTSDVEVNEKKDR					
HL65K	TKDETTIVEGAGD	TDALAGRVAQIRTEIENS	SDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHS					
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAM	TI	AKNAGVEGSLI					
HL65K	IEDAVRNAKA	AVEEGIVAGGGVTLLQAAPALDKLKL	TGDEAT-GANIVKVALEAPLKQIAFNSGMEPGV					
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEV	VVTEIPKEEKDPGMG						
HL65K	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTR	SALQNAASIAGLFTT-EAVVADKPEKTAAPASD						
	561	570						
HUMP1	MGGMG	GGMGGMGGMF						
HL65K	TGGMG	G-MD---F						

Total score = 4552, 7 breaks
 255 identities out of 540 possible matches between residues

25 random runs
 Alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.15

FIGURE 4

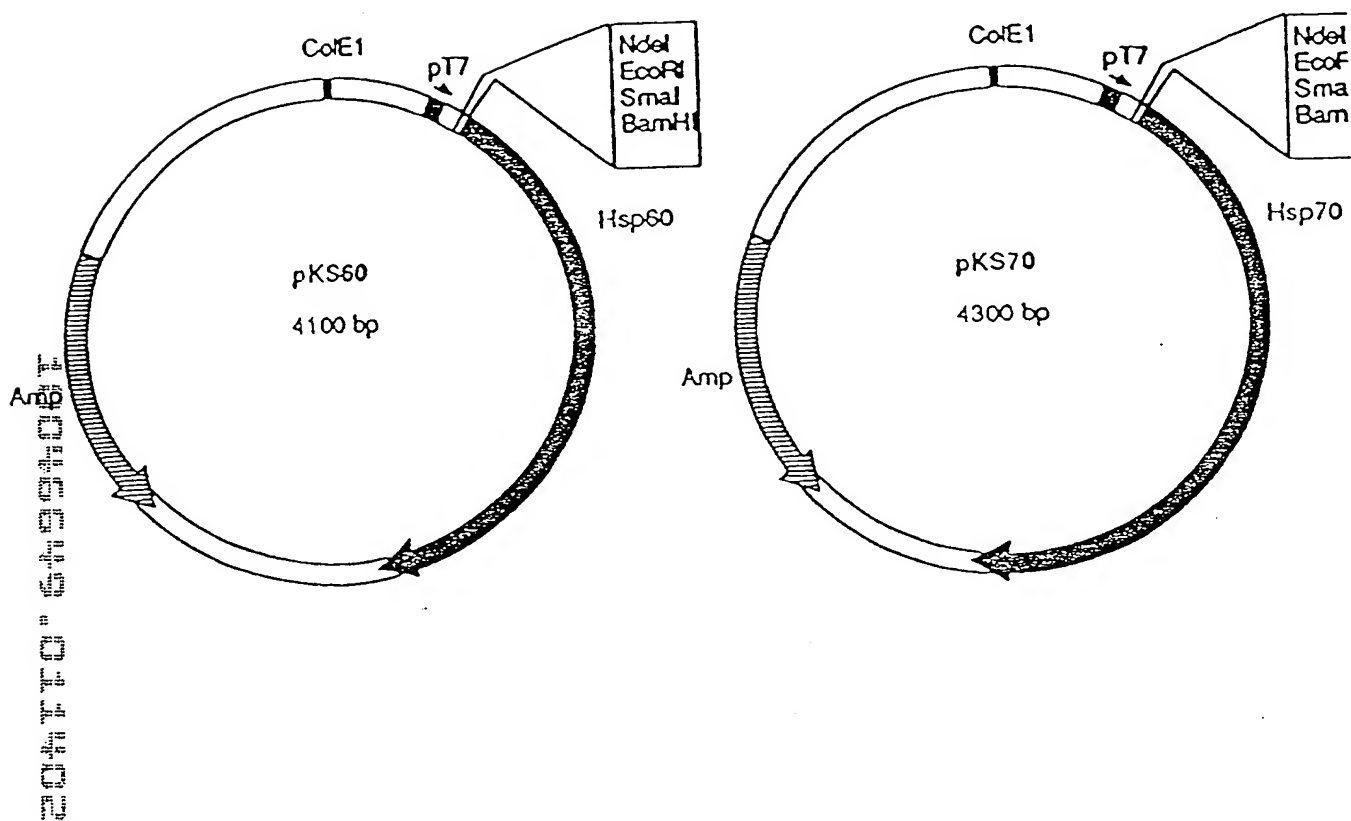
1 10 20 30 40 50 60 70
 HUMPI MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKEFGADARALMLQGVDLLADAVAVTMGPKGRTVIEEQSWGS
 TB65K M-----AKTIAYDEEARRGLERGLNALADAVKVTLGPKGRNVVLEKKWGA
 71 80 90 100 110 120 130 140
 HUMPI PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLRSLIAKEGFEXISKGANPVEI
 TB65K PTITNDGVSLIAKEIELEDPEYKIGAEELVKEVAKKTDDVAGDGTTTATVLAQALRKEGLRNVAAGANPLGI
 141 150 160 170 180 190 200 210
 HUMPI RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDANKKVGRKGVITVKDGKTLNDI
 TB65K KRGIEKAVEKVTETLLKGAKVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVTVEESNTFGLK
 211 220 230 240 250 260 270 280
 HUMPI LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHKPLVIAEDVDI
 TB65K LELTEGMRFDKGYISGYFVTDPERQEAVLEDPEYILLVSSKSVSTVKDLLPLEKVIAGKPLIIAEDVEI
 281 290 300 310 320 330 340 350
 HUMPI EALSTLVNRLKXVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGVTI
 TB65K EALSTLVNKRIGTFKSVAVKAPGFGDRRKAMLCMAILTGGQVISEE-VGLTLENADLSLLGKARKVV
 351 360 370 380 390 400 410 420
 HUMPI TKDDAMLLKGGDKAQIEKRIQEIIEQLDVTTSSEYEKEKLNRLAKLSDGVAVLKVGGTSDVEVNEKKD
 TB65K TKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKH
 421 430 440 450 460 470 480 490
 HUMPI VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIKRTLKIPAMTIKNAGVEGSI
 TB65K IEDAVRNAKAAVEEGIVAGGGVTLQAAPTLDLKL-LEGDEATGANIVKVALEAPLKQIAFNSGLEPGI
 491 500 510 520 530 540 550 560
 HUMPI VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGM
 TB65K AEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRESALQNAASIAGLFLTTEAVVADKPEKEKASVP
 561 570
 HUMPI MGGMGGGMGGGMF
 TB65K ----GGDMGGMDF

Total score - 4560, 5 breaks

257 identities out of 540 possible matches between residues

 25 random runs
 Alignment score - 49.36 SD Standard deviation - 23.23 Mean - 3413.16

Figure 5



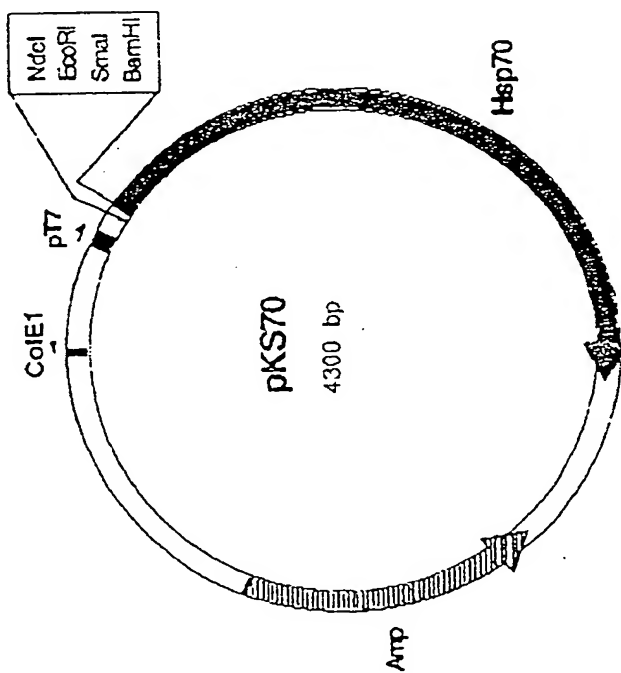
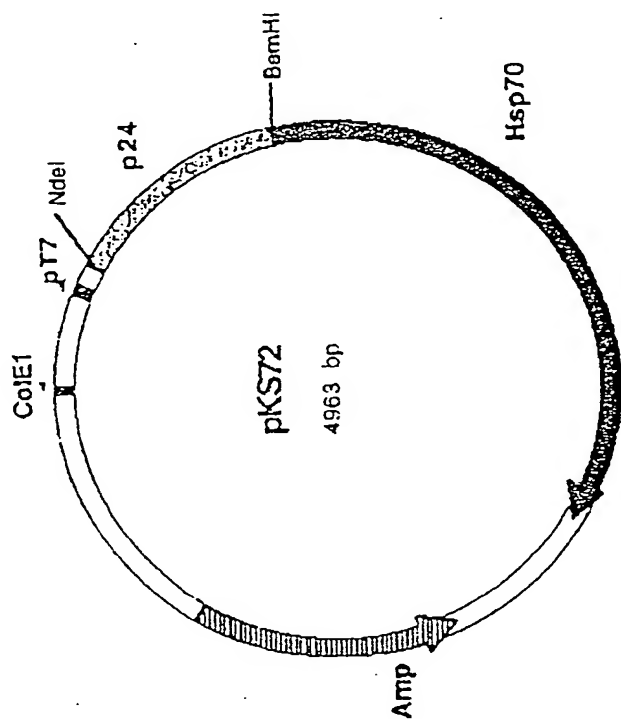


FIGURE 6

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[illegible]